

	9	18	27	36	45	54
5' GC CGC TCG CAC GCC CTT GGG CCG CCG GGC GCC GCC TTC CGC TTG						
	63	72	81	90	99	108
CGC TGT GAG CTG AGG CGG TGT ATG TGC GGC AAT AAC ATG TCA ACC CCG CTG CCC M C G N M S T P L P						
	117	126	135	144	153	162
GCC ATC GTG CCC GCC CGG AAG GCC ACC GCT GCG GTG ATT TTC CTG CAT GGA A I V P A A R K A T A A V I F L H G						
	171	180	189	198	207	216
TTC GGA GAT ACT GGG CCT GTT AGG CCT GTT ACA TTA AAT ATG AAC GTG GCT ATG L G D T G P V R P P V T L N N M N V A M						
	225	234	243	252	261	270
CCT TCA TGG TTT GAT ATT ATT GGG CTT TCA CCA GAT TCA CAG GAG GAT GAA TCT P S W F D I I I G L S P D S Q E D E S						
	279	288	297	306	315	324
GGG ATT AAA CAG GCA GCA GAA AAT ATA AAA GCT TTG ATT GAT CAA GAA GTG AAG G I K Q A A E N I K A A L I D Q E V K						

FIGURE 1A

333	342	351	360	369	378
AAT GGC ATT CCT TCT AAC AGA ATT TTG GGA GGG TTT TCT CAG GGA GGA GCT					
N G I P S N R I I L G G F S Q G G A					
387	396	405	414	423	432
TTA TCT TTA TAT ACT GCC CTT ACC ACA CAG CAG AAA CTG GCA GGT GTC ACT GCA					
L S L Y T A L T T Q Q K L A G V T A					
441	450	459	468	477	486
CTC AGT TTC TTG CTT CCA CTT CGG GNT TCC TTT CCA CAG GAK CCT ATC GGT GGT					
L S F L L P L R X S F P Q G P I G G					
495	504	513	522	531	540
GCT AAT AGA GAT ATT TCT ATT CTC CAG TGC CAC GGG GAT TGT GAC CCT TTG GTT					
A N R D I S I L Q C H G D C D P L V					
549	558	567	576	585	594
CCC CTG ATG TTT GGT TCT CTT ACG GTG GAA AAA CTA AAA ACA TTG GTG AAT CCA					
P L M F G S L T V E K L K T L V N P					
603	612	621	630	639	648
GCC AAT GTG ACC TTT AAA ACC TAT GAA GGT ATG CAC AGT TCG TGT CAA CAG					
A N V T F K T Y E G M M H S S C Q Q					

FIGURE 1B

657	GAA	ATG	ATG	GAT	GTC	AAG	CAA	TTC	ATT	GAT	AAA	CTC	CTA	CCT	CCA	ATT	GAT	TGA	702
	E	M	M	D	V	K	Q	F	I	D	K	L	L	P	P	I	I	D	
	CGT	CAC	TA	3'															
	R	H																	

FIGURE 1C

1	MC	GN	NM	ST	P	L	P	A	I	V	P	A	A	R	K	A	T	A	A	V	I	F	L	H	G	L	G	D	T	G	-	-	-	-	-	-	2676650				
1	MC	GN	NM	S	A	P	M	P	A	V	V	P	A	A	R	K	A	T	A	A	V	I	F	L	H	G	L	G	D	T	G	H	G	W	A	E	A	GI 1552244			
35	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2676650						
41	F	A	G	I	K	S	S	H	I	K	Y	I	C	P	H	A	P	V	M	P	V	T	L	N	M	S	M	M	P	S	W	F	D	I	I	G	L	S	P	GI 1552244	
59	D	S	Q	E	D	E	S	G	I	K	Q	A	A	E	N	I	K	A	L	I	D	Q	E	V	K	N	G	I	P	S	N	R	I	I	L	G	G	F	S	Q	2676650
81	D	S	Q	E	D	E	S	G	I	K	Q	A	A	E	T	V	K	A	L	I	D	Q	E	V	K	N	G	I	P	S	N	R	I	I	L	G	G	F	S	Q	GI 1552244
99	G	G	A	L	S	L	Y	T	A	L	T	T	Q	Q	K	L	A	G	V	T	A	L	S	F	L	L	P	L	R	X	S	F	P	Q	G	P	I	G	G	A	2676650
121	G	G	A	L	S	L	Y	T	A	L	T	T	Q	Q	K	L	A	G	V	T	A	L	S	C	W	L	P	L	R	A	S	F	S	Q	G	P	I	N	S	A	GI 1552244
139	N	R	D	I	S	I	L	Q	C	H	G	D	C	D	P	L	V	P	L	M	F	G	S	L	T	V	E	K	L	K	T	L	V	N	P	A	N	V	T	F	2676650
161	N	R	D	I	S	V	L	Q	C	H	G	D	C	D	P	L	V	P	L	M	F	G	S	L	T	V	E	R	L	K	G	L	V	N	P	A	N	V	T	F	GI 1552244
179	K	T	Y	E	G	M	M	H	S	S	C	Q	Q	E	M	M	D	V	K	Q	F	I	D	K	L	L	P	P	I	D								2676650			
201	K	V	Y	E	G	M	M	H	S	S	C	Q	Q	E	M	M	D	V	K	Y	F	I	D	K	L	L	P	P	I	D								GI 1552244			

FIGURE 2

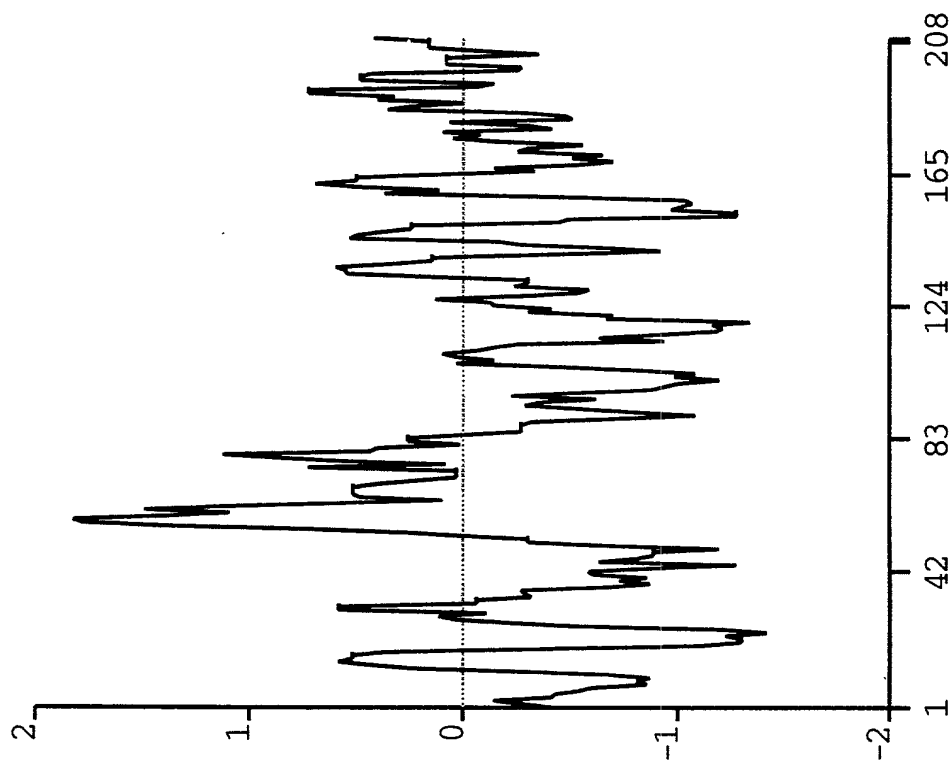


FIGURE 3A

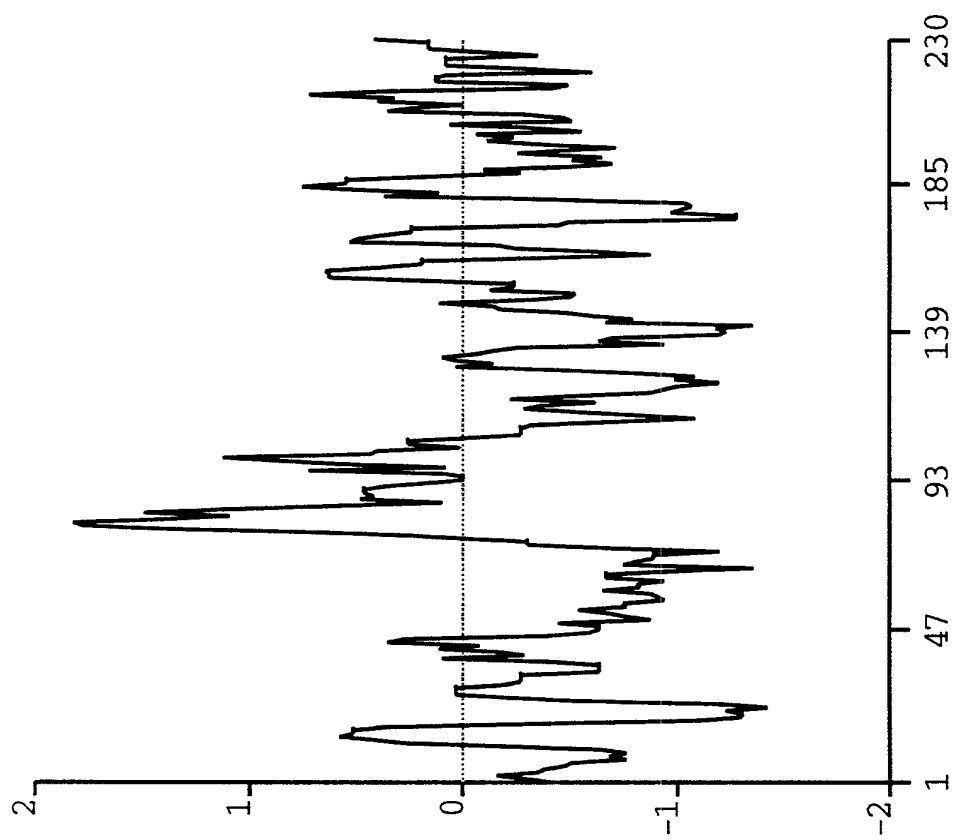


FIGURE 3B

Library	Lib Description	Abun	Pct Abun
U937NOT01	U937 monocyte cell line, 37 M	3	0.1491
COCHFEM01	ear, cochlea, fetal, WM	1	0.1157
RATRNOT01	heart, right atrium, 51 F	1	0.0874
OVARTUT04	ovarian tumor, 53 F	3	0.0755
TBLYNOT01	T-B lymphoblast cell line, leukemia	2	0.0652
PGANNOT03	paraganglionic tumor, benign paraganglioma, 46 M	2	0.0622
ENDCNOT01	endothelial cells, coronary artery, 58 M	2	0.0535
MPHGNOT03	macrophages (adher PBMC), M/F	4	0.0517
FIBRNOT01	WI38 lung fibroblast cell line, 3m F	1	0.0469
ADENINB01	adenoid, inflamed, 3y	2	0.0381
BLADNOT01	bladder, 78 F	1	0.0350
COLNNOT05	colon, 40 M, match to COLNCRT01	1	0.0289
UTRSNOT06	uterus, myometrium, 50 F	1	0.0282
BLADTUT07	bladder, microfoci tumor, 58 M	1	0.0278
HYPONOB01	hypothalamus, 16-75 M/F	1	0.0272
PROSNOT16	prostate, 68 M	2	0.0263
KIDNNOT19	kidney, 65 M	1	0.0259
COLNTUT16	colon tumor, 60 M, match to COLNNOT07/08/09/11	1	0.0256
THYRNOT09	thyroid, adenomatous goiter, 18 F	1	0.0254
HNT2AGT01	hNT2 cell line, post-mitotic neurons	1	0.0192
HNT3AZT01	hNT2 cell line, teratocarcinoma, treated AZ	1	0.0191
HNT2NOT01	hNT2 cell line, teratocarcinoma, untreated	1	0.0173
SINTBST01	small intestine, ileum, Crohn's, 18 F	1	0.0168
BEPINOT01	bronchial epithelium, primary cell line, 54 M	1	0.0144
BRSTTUT02	breast tumor, 54 F, match to BRSTNOT03	1	0.0140

FIGURE 4A

TESTTUT02	testicular tumor, 31 M	1	0.0134
CONUTUT01	mesenteric tumor, sigmoid, 61 F	1	0.0130
SINTFET03	small intestine, fetal F	1	0.0130
THP1NOT03	THP-1 promonocyte cell line, untreated	1	0.0129
PROSTUT04	prostate tumor, 57 M, match to PROSNOT06	1	0.0117
PLACNOM02	placenta, neonatal F, NORM, WM	2	0.0111
BRSTNOT04	breast, 62 F	1	0.0096
PROSNON01	prostate, 28 M, NORM	1	0.0094
BRAINOM01	brain, infant F, NORM, WM	2	0.0089
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0086
LUNGFET03	lung, fetal F	1	0.0069

FIGURE 4B